

A1
 ¶ Figures 6A-6E (SEQ ID NOS:3, 5, 7, 9, 11, 13, 15 and 17) show a DNA alignment created by PileUp and displayed by Pretty software (a component of the GCG Wisconsin Package, version 10, provided by the SeqWeb sequence analysis package, version 1.1, of the Canadian Bioinformatics Resource). The figure depicts the isolated nucleotide sequences of the *gapC* genes from *S. dysgalactiae* (DysGapC, Check 9344), *S. agalactiae* (AgalGapC, Check 2895), *S. uberis* (UberGapC, Check 5966), *S. parauberis* (PUberGapC, Check 9672), and *S. iniae* (IniaeGapC, Check 990). The previously known sequences of *S. equisimilis* (SeqGapC, Check 5841), *S. pyogenes* (SpyGapC, Check 4037), and a bovine GAPDH protein (BovGapC, check 5059) are also included. The length and weight parameters were the same for all sequences (1018 and 1.00, respectively). The parameters used in the DNA sequence comparison were as follows: Plurality--2.00; Threshold--1; AveWeight--1.00; AveMatch--1.00; AvMisMatch--0.00; Symbol comparison table--pileupdna.cmp; CompCheck--6876; GapWeight--5; GapLengthWeight--1; PileUp MSF--1018; Type--N; Check--3804. In the figure, dashes represent identical nucleotides; dots represent gaps introduced by the software used to generate the alignment chart, and tildes represent regions not included in the overall alignment due to differences in the length of the gene sequences. A

Please replace the paragraph beginning on page 8, line 18 with the following rewritten paragraph:

A2
 ¶ Figures 7A-7B (SEQ ID NOS:4, 6, 8, 10, 12, 14, 16 and 18) show an amino acid sequence alignment created by PileUp and displayed by Pretty (as above) that depicts the deduced amino acid sequences of the GapC proteins from *S. dysgalactiae* (DysGapC, Check 6731), *S. agalactiae* (AgalGapC, Check 1229), *S. uberis* (UberGapC, Check 8229), *S. parauberis* (PUberGapC, Check 8889) and *S. iniae* (IniaeGapC, check 8785). The previously known sequences of *S. equisimilis* (SeqGapC, Check 8252), *S. pyogenes* (SpyGapC, Check 6626) and a bovine GAPDH protein (BovGapC, Check 8479) are also included. In the figure, dashes represent identical amino acid residues;

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dots represent gaps introduced by the PileUp software, and tildes represent regions not included in the overall alignment due to differences in the length of the gene sequences. 4

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "**Version with markings to show changes made.**"

REMARKS

The foregoing amendments are made to insert the sequence identification numbers into the specification. No new matter has been added.

Respectfully submitted,

Date:

9/6/02

By:


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